TrueAllele® Release 2014a

## New and updated features in the 2014a release:

*General*

- Integrated VUIer™ software manuals via the new documentation installer
- Support for GlobalFiler™, IDplex, MiniFiler™, PowerPlex® 21 and PowerPlex® Fusion kits
- Support for 6-dye kits in all interfaces

*Analyze module*

- Enhanced color separation settings for ABI 310 genetic analyzer data

*Data module*

- Ability to upload multiple data *.gel* files in one batch

*Request module*

- Prioritized request processing that allows the analyst to set which requests should be interpreted first

*Review module*

- CODIS preferences file for cmf export, edited via the Tools module

*Report module*

- Updated the co-ancestry calculation. The previous version was more conservative. The current version is more accurate, and handles evidence-to-evidence comparisons.
- Additional specificity statistics
- KL statistics per locus for all genotypes

## Before you install the software

*Preserve your customized files and templates*

Cybergenetics recommends that you perform a clean installation of the Analyze and VUIer software. Before removing your current software, please preserve the following folders by copying these folders to another location. In doing so, you will preserve files that have been customized to your site.

| | Located in: | |
|---|---|---|
| | Mac | PC |
| Preferences | /Library/TrueAllele | /Program Files/VUIer |
| trueallele | /Documents | /My Documents (for every user) |

*Uninstall the current versions*

After preserving these files, it is safe to uninstall the software. Be sure to remove all files and folders when uninstalling the software.

*Verify that you are using the MATLAB 7.16 engine*

To install the 2014a versions, first verify that you have the MATLAB Engine 7.16 installed. You can check by opening the /MATLAB/MATLAB_Compiler_Runtime folder on your Viewstation and seeing if there's a folder inside named v716:

| | Located in: | |
|---|---|---|
| | Mac | PC |
| MATLAB | /Applications | /Program Files |

*Install Analyze and VUIer 2014a*

To install the 2014a VUIer and Analyze versions, please follow the Mac- or PC-specific instructions found in the **Getting Started** manual. Please contact Cybergenetics if you have any questions about installing the software.

*Replace customized Analyze files and templates, and update the Init Preferences*

Once Analyze is installed, copy the *operators.txt* and *db_prefs.txt* files from your preserved files back into the /trueallele/user directory. If your site uses a customized DataDisk template, move this template to the /trueallele/template directory.

Start Analyze and in the Command Window select Edit > Preferences > Init and reset your initial preferences.

*Replace customized VUIer files*

Once VUIer is installed, copy the *connect.txt* file from your preserved files into the VUIer Preferences folder. If you have customized other Preferences files, replace them as well.

*(Optional) Install VUIer Documentation*

To install the 2014a VUIer documentation, please follow the Mac- or PC-specific instructions found in the **Getting Started** manual. **Note**: VUIer and Analyze must be installed before installing the documentation. Please contact Cybergenetics if you have any questions about installing the manuals.